



- 1 -

SEQUENCE LISTING

<110> Vertino, Paula M.

<120> TMS1 Compositions and Methods of Use

<130> E0355/7003/ERG/MAT

<140> US 09/691,763

<141> 2000-10-18

<150> US 60/159,975

<151> 1999-10-18

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2821

<212> DNA

<213> Homo Sapiens

<400> 1

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tctgtcaccc	aggctggagt	gcagtgggtc	aatcttggct	cactgtagcc	tctgcctccg	180
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ccacacacag	ctatttccag	gtacattctt	gacgctagga	attcagcaaa	gaataagaca	300
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atataaacat	ataatatgtc	agggtcgtat	gactacaagg	aacagtgatt	gttacaaccc	420
agatgagagg	gaaaaataaaa	ggattccaaa	tatccccctt	gggaagtaga	gtcaggattc	480
aaacaaagaa	ctgtatggct	tcaagttcat	ggtctttaat	ctcctggagg	ctgtctctct	540
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gtcctggtgg	cgcgcccttg	gagccctgcc	cctaggcttg	cagaggaatt	cctgaagaac	2040
tcaagttcag	cagggacagg	ccccacaccc	tggctgctgg	ctcatgttct	cctcccaccc	2100

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ccaggcctgc actttataga ccagcaccgg      gctgcgctta tcgcgagggt cacaaacgtt
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cgggccgagc ccaccaaccc aagcaagatg cggaagctct tcagtttcac accagcctgg      2280
aactggacct gcaaggactt gtcctccag gccctaaggg agtcccagtc ctacctggtg      2340
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cccaccaaata catcctgaat ctgatctttt tatacacaat atacgaaaag ccagcttgaa      2460
cttgtgtgtt ttcttgcttc tagcctgctg gcatgtgcag agtcagcta tgcttcagag      2520
gccaccacagc ctccagctcc atgtccctag ggtctctggc accccaaatg cttcccccat      2580
ccttcctggt atcgccatgg aatatccctc ctcattcacc aggtggtgct cctccagtg      2640
tccctaaagg gtctaaccct accattatag ataacagcct gtgaccacag tccgaagggt      2700
aaaagaggca tgtaccaaag ggcgcaaact ggtgggcagc tctgtccaag ccatttagaa      2760
acacactagt cttcatagct cccctacctt ccacattttc cactggaaga aaaaatggca      2820
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<210> 2
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 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (75)...(662)

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gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg      110
          Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
                1                5                10

gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg      158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
          15                20                25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg      206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
          30                35                40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac      254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
          45                50                55                60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg      302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
          65                70                75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc      350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
          80                85                90

tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc      398
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
          95                100                105

aag cca ggc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg      446
Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala
          110                115                120

agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc      494
Arg Val Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val
          125                130                135                140

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ctg acg gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca 542
Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro
145 150 155

agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc 590
Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr
160 165 170

tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg 638
Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu
175 180 185

gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc 692
Val Glu Asp Leu Glu Arg Ser *
190 195

cctggcaatc ccaccaaata atcctgaatc tgatcttttt atacacaata tacgaaaagc 752
cagcttgaaa aaaaaaaaaa 770

<210> 3
<211> 195
<212> PRT
<213> Homo Sapiens

<400> 3
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1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
85 90 95
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu
100 105 110
His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn
115 120 125
Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu
130 135 140
Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg
145 150 155 160
Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu
165 170 175
Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu
180 185 190
Glu Arg Ser
195

<210> 4
<211> 626
<212> DNA
<213> Homo Sapiens

<400> 4
agcgcctttt gctggagggc aacggaccgg ggcggggagt cgggagacca gaggggagg 60
aagcggggga gtccaggttc cgccccggag ccgacttcct cctggtcggc ggctgcagcg 120

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gggtgagcgg cggcagcggc cggggatcct      ggagccatgg ggcgcgcgcg cgacgccatc
180
ctggatgcgc tggagaacct gaccgccgag gagctcaaga agttcaagct gaagctgctg      240
tcggtgccgc tgcgcgaggg ctacggggcg atcccgcggg gcgcgctgct gtccatggac      300
gccttggaac tcaccgacaa gctggtcagc ttctacctgg agacctacgg cgccgagctc      360
accgctaacg tgctgcgcga catgggctg caggagatgg cggggcagct gcaggcggcc      420
acgcaccagg gtgagccgcc cccgttcccc tccaccccg ctttcccctc caccacacc      480
agcgcttacc ccgcgggctc ttccgcttcc tgttctctct acccctaaac aaagctgctc      540
taccgaaaag gaggtcctcc acgcttgccc taccgaccaa cgggaccccg gccccacggc      600
gggaagggaa gggaagggga tcactt      626

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<210> 5
 <211> 340
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (67)...(339)

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<400> 5
ccgacttcct cctggtcggc ggctgcagcg gggtgagcgg cggcagcggc cggggatcct      60
ggagcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg gag aac      108
      Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
        1             5             10

ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tcg gtg      156
Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val
      15             20             25             30

ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg ctg tcc      204
Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
              35             40             45

atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag      252
Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
              50             55             60

acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg ggc ctg      300
Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
              65             70             75

cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g      340
Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
      80             85             90

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<210> 6
 <211> 91
 <212> PRT
 <213> Homo Sapiens

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<400> 6
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
  1             5             10             15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
      20             25             30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Ser Met Asp
      35             40             45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
      50             55             60

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Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
 65 70 75 80
 Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
 85 90

<210> 7
 <211> 57
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (3)...(56)

<400> 7
 gc tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca 47
 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala
 1 5 10 15
 gcc aag cca g 57
 Ala Lys Pro

<210> 8
 <211> 18
 <212> PRT
 <213> Homo Sapiens

<400> 8
 Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
 1 5 10 15
 Lys Pro

<210> 9
 <211> 356
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS
 <222> (3)...(258)

<400> 9
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 Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val
 1 5 10 15
 aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg 95
 Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr
 20 25 30
 gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag 143
 Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys
 35 40 45
 atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag 191
 Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys
 50 55 60

gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag 239
 Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu
 65 70 75

gac ctg gag cgg agc tga g gctccttccc agcaacactc cggtcagccc 288
 Asp Leu Glu Arg Ser *
 80

ctggcaatcc caccaaatca tcctgaatct gatcttttta tacacaatat acgaaaagcc 348
 agcttgaa 356

<210> 10
 <211> 84
 <212> PRT
 <213> Homo Sapiens

<400> 10
 Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
 1 5 10 15
 Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
 20 25 30
 Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
 35 40 45
 Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
 50 55 60
 Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
 65 70 75 80
 Leu Glu Arg Ser

<210> 11
 <211> 18
 <212> DNA
 <213> Homo Sapiens

<400> 11
 gcactttata gaccagca 18

<210> 12
 <211> 18
 <212> DNA
 <213> Homo Sapiens

<400> 12
 atttggtggg attgccag 18

<210> 13
 <211> 17
 <212> DNA
 <213> Homo Sapiens

<400> 13
 tgggcctgca ggagatg 17

<210> 14
 <211> 22
 <212> DNA
 <213> Homo Sapiens

<400> 14
 ccttcctggg catggagtcc tg 22

<210> 15
<211> 21
<212> DNA
<213> Homo Sapiens

<400> 15
ggagcaatga tcttgatctt c 21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 16
ggttgtagtg gggtagtg t 21

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Primer

<400> 17
caaaacatcc ataaacaaca acaca 25

<210> 18
<211> 19
<212> DNA
<213> Homo Sapiens

<400> 18
ttgtagcggg gtgagcggc 19

<210> 19
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 19
aacgtccata aacaacaacg cg 22

<210> 20
<211> 803
<212> DNA
<213> Mus Musculus

<220>
<221> CDS
<222> (162)...(743)

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aagcagctga ctctctggtc ttggcgggct ggcagcaggc aggctgagca ggcgagcagc 120
agcaagagta aaaggtgacc gcggctgccc accccagagc c atg ggg cgg gca cga 176
Met Gly Arg Ala Arg

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gat gcc atc ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa      224
Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys
      10                      15                      20

aag ttc aag atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg      272
Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly
      25                      30                      35

cgc atc cca cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act      320
Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr
      40                      45                      50

gac aaa ctt gtc agc tac tat ctg gag tgc tat ggc ttg gag ctc aca      368
Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr
      55                      60                      65

atg act gtg ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg      416
Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu
      70                      75                      80                      85

caa acg act aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc      464
Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala Ala Ala Ala Ser Val
      90                      95                      100

cct gct cag agt aca gcc aga aca gga cac ttt gtg gac cag cac agg      512
Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg
      105                      110                      115

caa gca ctc att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct      560
Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala
      120                      125                      130

ttg cat ggc agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca      608
Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala
      135                      140                      145

gag acc acc agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca      656
Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro
      150                      155                      160                      165

tcc tgg aac ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa      704
Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu
      170                      175                      180

ata cat ccc tac ttg gtg atg gac ctg gag cag agc tga ggtatctttt      753
Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln Ser *
      185                      190

ccagctacat tatctagctc ctgactttgt atacacaatt tttgaaaaaa      803

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<210> 21
<211> 193
<212> PRT
<213> Mus Musculus

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<400> 21
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser
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Gly Asp Glu Leu Lys Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu

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[illegible]

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<210> 22
<211> 605
<212> DNA
<213> Rattus Norvegicus
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<220>  
<221> CDS  
<222> (2) ... (518)
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	Phe	Lys	Ile	Lys	Leu	Leu	Thr	Ala	Pro	Val	Arg	Glu	Gly	Tyr	Gly	Arg	
	1				5					10					15		
atc	cca	cgg	ggg	gcc	ctg	ctg	cag	atg	gac	ccc	ata	gac	ctc	act	gat	97	
Ile	Pro	Arg	Gly	Ala	Leu	Leu	Gln	Met	Asp	Pro	Ile	Asp	Leu	Thr	Asp		
			20					25					30				
aaa	ctc	gtc	agy	tac	tat	ctg	gag	ggg	tat	ggc	ttg	gag	ctc	aca	atg	145	
Lys	Leu	Val	Xaa	Tyr	Tyr	Leu	Glu	Gly	Tyr	Gly	Leu	Glu	Leu	Thr	Met		
		35					40					45					
act	gtg	ctt	aga	gac	atg	ggc	ata	cag	gag	ctg	gct	gag	cag	ctg	caa	193	
Thr	Val	Leu	Arg	Asp	Met	Gly	Ile	Gln	Glu	Leu	Ala	Glu	Gln	Leu	Gln		
	50					55					60						
aag	att	atg	gaa	gag	tct	gga	gct	gtg	gct	act	gca	acc	agt	gtc	cct	241	
Lys	Ile	Met	Glu	Glu	Ser	Gly	Ala	Val	Ala	Thr	Ala	Thr	Ser	Val	Pro		
65					70					75				80			
gct	cag	ggc	aca	gcc	aga	aca	gaa	cat	ttt	gtg	gac	caa	cac	agg	caa	289	
Ala	Gln	Gly	Thr	Ala	Arg	Thr	Glu	His	Phe	Val	Asp	Gln	His	Arg	Gln		
				85					90					95			
gca	ctc	att	gcc	agg	gtc	aca	gaa	gtt	gat	ggt	ttg	ctg	gat	gct	ctg	337	
Ala	Leu	Ile	Ala	Arg	Val	Thr	Glu	Val	Asp	Gly	Leu	Leu	Asp	Ala	Leu		
			100					105					110				

tat ggc aat gtg ctg act gaa gga cag tac cag gca gtt cgt gca gag	385
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu	
115 120 125	

acc acc aac caa aac aag atg agg aag ctc ttt agc ttt gct cca gcc	433
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala	
130 135 140	

tgg aac ctg acc tgc aag aac ttg ttc ctt gag gcc ttg agg caa aca	481
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr	
145 150 155 160	

cag ccc tac ttg gtg aca gac ctg gaa cag agc tga g gtatcttttc	528
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser *	
165 170	

cagctacaca tctagctcct gggtttgtat acaaaatttt ctaaaaacaa gtttgtattt	588
gtgttttctc gaaaaaa	605

<210> 23
 <211> 171
 <212> PRT
 <213> Rattus Norvegicus

<220>
 <223> Xaa can be any amino acid.

<400> 23	
Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg	
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Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp	
20 25 30	
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met	
35 40 45	
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln	
50 55 60	
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro	
65 70 75 80	
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln	
85 90 95	
Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu	
100 105 110	
Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu	
115 120 125	
Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala	
130 135 140	
Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr	
145 150 155 160	
Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser	
165 170	

<210> 24
 <211> 713
 <212> DNA
 <213> Homo Sapiens

<220>
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 <222> (75)...(605)

<400> 24
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gggatcctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
1 5 10

gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
15 20 25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
65 70 75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
80 85 90

ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc aca 398
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
95 100 105

aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg gat 446
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
110 115 120

gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag atg 494
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
125 130 135 140

cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag gac 542
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
145 150 155

ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag gac 590
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
160 165 170

ctg gag cgg agc tga ggctccttcc cagcaacact ccggtcagcc cctggcaatc 645
Leu Glu Arg Ser *
175

ccaccaaata atcctgaata tgatcttttt atacacaata tacgaaaagc cagcttgaaa 705
aaaaaaaa 713

<210> 25

<211> 176

<212> PRT

<213> Homo Sapiens

<400> 25

Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
1 5 10 15

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			20					25				30				
Arg	Glu	Gly	Tyr	Gly	Arg	Ile	Pro	Arg	Gly	Ala	Leu	Leu	Ser	Met	Asp	
		35					40					45				
Ala	Leu	Asp	Leu	Thr	Asp	Lys	Leu	Val	Ser	Phe	Tyr	Leu	Glu	Thr	Tyr	
		50				55					60					
Gly	Ala	Glu	Leu	Thr	Ala	Asn	Val	Leu	Arg	Asp	Met	Gly	Leu	Gln	Glu	
65					70					75					80	
Met	Ala	Gly	Gln	Leu	Gln	Ala	Ala	Thr	His	Gln	Gly	Leu	His	Phe	Ile	
			85						90					95		
Asp	Gln	His	Arg	Ala	Ala	Leu	Ile	Ala	Arg	Val	Thr	Asn	Val	Glu	Trp	
			100					105					110			
Leu	Leu	Asp	Ala	Leu	Tyr	Gly	Lys	Val	Leu	Thr	Asp	Glu	Gln	Tyr	Gln	
		115					120					125				
Ala	Val	Arg	Ala	Glu	Pro	Thr	Asn	Pro	Ser	Lys	Met	Arg	Lys	Leu	Phe	
		130				135					140					
Ser	Phe	Thr	Pro	Ala	Trp	Asn	Trp	Thr	Cys	Lys	Asp	Leu	Leu	Leu	Gln	
145					150					155					160	
Ala	Leu	Arg	Glu	Ser	Gln	Ser	Tyr	Leu	Val	Glu	Asp	Leu	Glu	Arg	Ser	
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 <213> Homo Sapiens

<220>
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 <222> (75)...(404)

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gggatcctgg	agcc	atg ggg cgc gcg cgc	gac gcc atc	ctg gat gcg	ctg		110								
	Met	Gly Arg Ala Arg	Asp Ala Ile	Leu Asp	Ala Leu										
	1		5		10										
gag aac ctg	acc gcc gag	gag ctc aag	aag ttc aag	ctg aag	ctg ctg		158								
Glu Asn Leu	Thr Ala Glu	Glu Leu Lys	Lys Phe Lys	Leu Lys	Leu Leu										
	15		20		25										
tcg gtg ccg	ctg cgc gag	ggc tac ggg	cgc atc ccg	ccg ggc	gcg ctg		206								
Ser Val Pro	Leu Arg Glu	Gly Tyr Gly	Arg Ile Pro	Arg Gly	Ala Leu										
	30		35		40										
ctg tcc atg	gac gcc ttg	gac ctc acc	gac aag ctg	gtc agc	ttc tac		254								
Leu Ser Met	Asp Ala Leu	Asp Leu Thr	Asp Lys Leu	Val Ser	Phe Tyr										
	45		50		55		60								
ctg gag acc	tac ggc gcc	gag ctc acc	gct aac gtg	ctg cgc	gac atg		302								
Leu Glu Thr	Tyr Gly Ala	Glu Leu Thr	Ala Asn Val	Leu Arg	Asp Met										
		65		70	75										
ggc ctg cag	gag atg gcc	ggg cag ctg	cag gcg gcc	acg cac	cag ggc		350								
Gly Leu Gln	Glu Met Ala	Gly Gln Leu	Gln Ala Ala	Thr His	Gln Gly										
	80		85		90										
tct gga gcc	gcg cca gct	ggg atc cag	gcc cct cct	cag tcg	gca gcc		398								
Ser Gly Ala	Ala Pro Ala	Gly Ile Gln	Ala Pro Pro	Gln Ser	Ala Ala										
	95		100		105										
aag cca g							405								

Lys Pro
110

<210> 27
<211> 110
<212> PRT
<213> Homo Sapiens

<400> 27
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr
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Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
85 90 95
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro
100 105 110